SEQUENCE LISTING

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<110> Koffas, Mattheos
      Odom, J. Martin
      Schenzle, Andreas J.
      Norton, Kelley C.
      Tomb, Jean-Francois
      Rouviere, Pierre
      Picataggio, Stephen
      Cheng, Qiong
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35 40 45

Phe Ala Ala Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr
50 55 60

Val Phe Asn Thr Pro Val Asp Gln Leu Val Trp Asp Val Gly His Gln 65 70 75 80

Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Lys Glu Arg Met Pro Thr 85 90 95

Ile Arg Thr Leu Gly Gly Val Ser Ala Phe Pro Ala Arg Asp Glu Ser 100 105 110

Glu Tyr Asp Ala Phe Gly Val Gly His Ser Ser Thr Ser Ile Ser Ala 115 120 125

Ala Leu Gly Met Ala Ile Ala Ser Gln Leu Arg Gly Glu Asp Lys Lys 130 135 140

Met Val Ala Ile Ile Gly Asp Gly Ser Ile Thr Gly Gly Met Ala Tyr 145 150 155 160

Glu Ala Met Asn His Ala Gly Asp Val Asn Ala Asn Leu Leu Val Ile 165 170 175

Leu Asn Asp Asn Asp Met Ser Ile Ser Pro Pro Val Gly Ala Met Asn 180 185 190

Asn Tyr Leu Thr Lys Val Leu Ser Ser Lys Phe Tyr Ser Ser Val Arg 195 200 205

Glu Glu Ser Lys Lys Ala Leu Ala Lys Met Pro Ser Val Trp Glu Leu 210 215 220 Ala Arg Lys Thr Glu Glu His Val Lys Gly Met Ile Val Pro Gly Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Phe Gly Pro Ile Asp Gly His Asp Val Glu Met Leu Val Ser Thr Leu Glu Asn Leu Lys Asp Leu Thr 265 Gly Pro Val Phe Leu His Val Val Thr Lys Lys Gly Lys Gly Tyr Ala Pro Ala Glu Lys Asp Pro Leu Ala Tyr His Gly Val Pro Ala Phe Asp Pro Thr Lys Asp Phe Leu Pro Lys Ala Ala Pro Ser Pro His Pro Thr Tyr Thr Glu Val Phe Gly Arg Trp Leu Cys Asp Met Ala Ala Gln Asp Glu Arg Leu Leu Gly Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Leu Val Glu Phe Ser Gln Lys Phe Pro Asn Arg Tyr Phe Asp Val Ala Ile Ala Glu Gln His Ala Val Thr Leu Ala Ala Gly Gln Ala Cys Gln Gly Ala Lys Pro Val Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Gly Tyr 395 Asp Gln Leu Ile His Asp Val Ala Leu Gln Asn Leu Asp Met Leu Phe 410 Ala Leu Asp Arg Ala Gly Leu Val Gly Pro Asp Gly Pro Thr His Ala 425 420 Gly Ala Phe Asp Tyr Ser Tyr Met Arg Cys Ile Pro Asn Met Leu Ile 440 Met Ala Pro Ala Asp Glu Asn Glu Cys Arg Gln Met Leu Thr Thr Gly 455 Phe Gln His His Gly Pro Ala Ser Val Arg Tyr Pro Arg Gly Lys Gly 470 475 Pro Gly Ala Ala Ile Asp Pro Thr Leu Thr Ala Leu Glu Ile Gly Lys 485 490 495 Ala Glu Val Arg His His Gly Ser Arg Ile Ala Ile Leu Ala Trp Gly 505 Ser Met Val Thr Pro Ala Val Glu Ala Gly Lys Gln Leu Gly Ala Thr 515 520 Val Val Asn Met Arg Phe Val Lys Pro Phe Asp Gln Ala Leu Val Leu

540

535

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getteeggtg geceattteg acggacgeg atagaaacgt tgtecaqcgt cacqccqqat
                                                                    600
caggccgttg cccatcctaa atgggacatg gggcgcaaga tttcggtcga ttccgccacc
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- Leu Thr Ala Asn Gly Asn Ile Asp Ala Leu Tyr Glu Gln Cys Leu Ala
 35 40 45
- His His Pro Glu Tyr Ala Val Val Met Glu Ser Lys Val Ala Glu 50 55 60
- Phe Lys Gln Arg Ile Ala Ala Ser Pro Val Ala Asp Ile Lys Val Leu 65 70 75 80
- Ser Gly Ser Glu Ala Leu Gln Gln Val Ala Thr Leu Glu Asn Val Asp 85 90 95
- Thr Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu
 100 105 110
- Ala Ala Lys Ala Gly Lys Thr Val Leu Leu Ala Asn Lys Glu Ala 115 120 125
- Leu Val Met Ser Gly Gln Ile Phe Met Gln Ala Val Ser Asp Ser Gly
 130 135 140
- Ala Val Leu Leu Pro Ile Asp Ser Glu His Asn Ala Ile Phe Gln Cys 145 150 155 160
- Met Pro Ala Gly Tyr Thr Pro Gly His Thr Ala Lys Gln Ala Arg Arg 165 170 175
- Ile Leu Leu Thr Ala Ser Gly Gly Pro Phe Arg Arg Thr Pro Ile Glu 180 185 190
- Thr Leu Ser Ser Val Thr Pro Asp Gln Ala Val Ala His Pro Lys Trp 195 200 205
- Asp Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr Met Met Asn Lys 210 215 220
- Gly Leu Glu Leu Ile Glu Ala Cys Leu Leu Phe Asn Met Glu Pro Asp 225 230 235 240
- Gln Ile Glu Val Val Ile His Pro Gln Ser Ile Ile His Ser Met Val 245 250 255
- Asp Tyr Val Asp Gly Ser Val Leu Ala Gln Met Gly Asn Pro Asp Met 260 265 270
- Arg Thr Pro Ile Ala His Ala Met Ala Trp Pro Glu Arg Phe Asp Ser
- Gly Val Ala Pro Leu Asp Ile Phe Glu Val Gly His Met Asp Phe Glu 290 295 300
- Lys Pro Asp Leu Lys Arg Phe Pro Cys Leu Arg Leu Ala Tyr Glu Ala 305 310 315 320
- Ile Lys Ser Gly Gly Ile Met Pro Thr Val Leu Asn Ala Ala Asn Glu 325 330 335

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Ala Val Ile Ile Glu Arg Ser Met Ala Gln Phe Lys Pro Asp Asp Ala
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ctgactcgac tacttgagtc cgacgccttc caaaaagttg cggtggcgat ttccgtcgaa 180
gaccettatt ggcetgaact gtecatagee aaacaceeg acateateae egegeetgge 240
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<213> Methylomonas 16a
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Ala Phe Gln Lys Val Ala Val Ala Ile Ser Val Glu Asp Pro Tyr Trp
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Pro Glu Leu Ser Ile Ala Lys His Pro Asp Ile Ile Thr Ala Pro Gly
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70

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Asp Ile Ala Ser Glu Asn Asp Trp Val Leu Val His Asp Ala Ala Arg
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Pro Cys Leu Thr Gly Ser Asp Ile His Leu Gln Ile Asp Thr Leu Lys
Asn Asp Pro Val Gly Gly Ile Leu Ala Leu Ser Ser His Asp Thr Leu
                        135
Lys His Val Asp Gly Asp Thr Ile Thr Ala Thr Ile Asp Arg Lys His
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Val Trp Arg Ala Leu Thr Pro Gln Met Phe Lys Tyr Gly Met Leu Arg
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Asp Ala Leu Gln Arg Thr Glu Gly Asn Pro Ala Val Thr Asp Glu Ala
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Ser Ala Leu Glu Leu Leu Gly His Lys Pro Lys Ile Val Glu Gly Arg
Pro Asp Asn Ile Lys Ile Thr Arg Pro Glu Asp Leu Ala Leu Ala Gln
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- <212> PRT
- <213> Methylomonas 16a
- <220>
- <223> Amino acid sequences encoded by ORF4
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- Leu Leu Gln Thr Val Phe Gln Met Leu Asp Leu Cys Asp Trp Leu Thr 35 40 45
- Phe His Pro Val Asp Asp Gly Arg Val Thr Leu Arg Asn Pro Ile Ser 50 60
- Gly Val Pro Glu Gln Asp Asp Leu Thr Val Arg Ala Ala Asn Leu Leu 65 70 75 80
- Lys Ser His Thr Gly Cys Val Arg Gly Val Cys Ile Asp Ile Glu Lys 85 90 95
- Asn Leu Pro Met Gly Gly Gly Leu Gly Gly Gly Ser Ser Asp Ala Ala 100 105 110
- Thr Thr Leu Val Val Leu Asn Arg Leu Trp Gly Leu Gly Leu Ser Lys 115 120 125
- Arg Glu Leu Met Asp Leu Gly Leu Arg Leu Gly Ala Asp Val Pro Val 130 135 140
- Phe Val Phe Gly Cys Ser Ala Trp Gly Glu Gly Val Ser Glu Asp Leu 145 150 155 160
- Gln Ala Ile Thr Leu Pro Glu Gln Trp Phe Val Ile Ile Lys Pro Asp 165 170 175
- Cys His Val Asn Thr Gly Glu Ile Phe Ser Ala Glu Asn Leu Thr Arg 180 185 190
- Asn Ser Ala Val Val Thr Met Ser Asp Phe Leu Ala Gly Asp Asn Arg 195 200 205
- Asn Asp Cys Ser Glu Val Val Cys Lys Leu Tyr Arg Pro Val Lys Asp 210 215 220
- Ala Ile Asp Ala Leu Leu Cys Tyr Ala Glu Ala Arg Leu Thr Gly Thr 225 230 235 240
- Gly Ala Cys Val Phe Ala Gln Phe Cys Asn Lys Glu Asp Ala Glu Ser 245 250 255
- Ala Leu Glu Gly Leu Lys Asp Arg Trp Leu Val Phe Leu Ala Lys Gly 260 265 270
- Leu Asn Gln Ser Ala Leu Tyr Lys Lys Leu Glu Gln Gly 275 280 285

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Ile Leu Gly Ala Ala Ala Leu Gly Asp Ile Gly Lys His Phe Pro Asp
                         55
Thr Asp Pro Asn Phe Lys Gly Ala Asp Ser Arg Val Leu Leu Arg His
                     70
Val Tyr Gly Ile Val Lys Glu Lys Gly Tyr Lys Leu Val Asn Ala Asp
                                     90
Val Thr Ile Ile Ala Gln Ala Pro Lys Met Leu Pro His Val Pro Gly
            100
                                105
                                                    110
Met Arg Ala Asn Ile Ala Ala Asp Leu Glu Thr Asp Val Asp Phe Ile
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<213> Methylomonas 16a
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Gly Thr Met Ser Pro Phe Gln His Gly Glu Val Phe Val Thr Glu Asp
     50
                         55
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- Gly Ala Glu Thr Asp Leu Asp Leu Gly His Tyr Glu Arg Phe Leu Lys
 65 70 75 80
- Thr Thr Met Thr Lys Lys Asn Asn Phe Thr Thr Gly Gln Val Tyr Glu 85 90 95
- Gln Val Leu Arg Asn Glu Arg Lys Gly Asp Tyr Leu Gly Ala Thr Val
- Gln Val Ile Pro His Ile Thr Asp Glu Ile Lys Arg Arg Val Tyr Glu 115 120 125
- Ser Ala Glu Gly Lys Asp Val Ala Leu Ile Glu Val Gly Gly Thr Val 130 135 140
- Gly Asp Ile Glu Ser Leu Pro Phe Leu Glu Thr Ile Arg Gln Met Gly
 145 150 155 160
- Val Glu Leu Gly Arg Asp Arg Ala Leu Phe Ile His Leu Thr Leu Val 165 170 175
- Pro Tyr Ile Lys Ser Ala Gly Glu Leu Lys Thr Lys Pro Thr Gln His
 180 185 190
- Ser Val Lys Glu Leu Arg Thr Ile Gly Ile Gln Pro Asp Ile Leu Ile 195 200 205
- Cys Arg Ser Glu Gln Pro Ile Pro Ala Ser Glu Arg Arg Lys Ile Ala 210 215 220
- Leu Phe Thr Asn Val Ala Glu Lys Ala Val Ile Ser Ala Ile Asp Ala 225 230 235 240
- Asp Thr Ile Tyr Arg Ile Pro Leu Leu Leu Arg Glu Gln Gly Leu Asp 245 250 255
- Asp Leu Val Val Asp Gln Leu Arg Leu Asp Val Pro Ala Ala Asp Leu 260 265 270
- Ser Ala Trp Glu Lys Val Val Asp Gly Leu Thr His Pro Thr Asp Glu 275 280 285
- Val Ser Ile Ala Ile Val Gly Lys Tyr Val Asp His Thr Asp Ala Tyr 290 295 300
- Lys Ser Leu Asn Glu Ala Leu Ile His Ala Gly Ile His Thr Arg His 305 310 315 320
- Lys Val Gln Ile Ser Tyr Ile Asp Ser Glu Thr Ile Glu Ala Glu Gly
 325 330 335
- Thr Ala Lys Leu Lys Asn Val Asp Ala Ile Leu Val Pro Gly Gly Phe 340 345 350
- Gly Glu Arg Gly Val Glu Gly Lys Ile Ser Thr Val Arg Phe Ala Arg
- Glu Asn Lys Ile Pro Tyr Leu Gly Ile Cys Leu Gly Met Gln Ser Ala 370 375 380

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Val Ile Glu Phe Ala Arg Asn Val Val Gly Leu Glu Gly Ala His Ser
385
                    390
                                        395
                                                            400
Thr Glu Phe Leu Pro Lys Ser Pro His Pro Val Ile Gly Leu Ile Thr
                405
                                    410
Glu Trp Met Asp Glu Ala Gly Glu Leu Val Thr Arg Asp Glu Asp Ser
            420
                                425
Asp Leu Gly Gly Thr Met Arg Leu Gly Ala Gln Lys Cys Arg Leu Lys
Ala Asp Ser Leu Ala Phe Gln Leu Tyr Gln Lys Asp Val Ile Thr Glu
Arg His Arg His Arg Tyr Glu Phe Asn Asn Gln Tyr Leu Lys Gln Leu
                                        475
Glu Ala Ala Gly Met Lys Phe Ser Gly Lys Ser Leu Asp Gly Arg Leu
                                    490
Val Glu Ile Ile Glu Leu Pro Glu His Pro Trp Phe Leu Ala Cys Gln
                                505
Phe His Pro Glu Phe Thr Ser Thr Pro Arg Asn Gly His Ala Leu Phe
                            520
Ser Gly Phe Val Glu Ala Ala Lys His Lys Thr Gln Gly Thr Ala
    530
                        535
<210> 13
<211> 891
<212> DNA
<213> Methylomonas 16a
<220>
<223> ORF7
<400> 13
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gcccgtctgc ctgccgaaaa catactgcca caaaccttgc atcaggccat gcgctattcc 120
gtattgaacg gcggcaaacg cacccggccc ttgttgactt atgcgaccgg tcaggctttg 180
ggcttgccgg aaaacgtgct ggatgcgccg gcttgcgcgg tagaattcat ccatgtgtat 240
togotgatto acgacgatot googgocatg gacaacgatg atotgogoog oggoaaaccg 300
acctgtcaca aggcttacga cgaggccacc gccattttgg ccggcgacgc actgcaggcg 360
ctggcctttg aagttctggc caacgacccc ggcatcaccg tcgatgcccc ggctcgcctg 420
aaaatgatca cggctttgac ccgcgccagc ggctctcaag gcatggtggg cggtcaagcc 480
ategateteg geteegtegg cegeaaattg acgetgeegg aactegaaaa catgeatate 540
cacaagactg gcgccctgat ccgcgccagc gtcaatctgg cggcattatc caaacccgat 600
ctggatactt gcgtcgccaa gaaactggat cactatgcca aatgcatagg cttgtcgttc 660
caggtcaaag acgacattct cgacatcgaa gccgacaccg cgacactcgg caagactcag 720
ggcaaggaca tcgataacga caaaccgacc taccctgcgc tattgggcat ggctggcgcc 780
aaacaaaaag cccaggaatt gcacgaacaa gcagtcgaaa gcttaacggg atttggcagc 840
gaagccgacc tgctgcgcga actatcgctt tacatcatcg agcgcacgca c
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<210> 14 <211> 297

- <212> PRT
- <213> Methylomonas 16a
- <220>
- <223> Amino acid sequences encoded by ORF7
- <400> 14
- Met Ser Lys Leu Lys Ala Tyr Leu Thr Val Cys Gln Glu Arg Val Glu
 1 5 10 15
- Arg Ala Leu Asp Ala Arg Leu Pro Ala Glu Asn Ile Leu Pro Gln Thr 20 25 30
- Leu His Gln Ala Met Arg Tyr Ser Val Leu Asn Gly Gly Lys Arg Thr 35 40 45
- Arg Pro Leu Leu Thr Tyr Ala Thr Gly Gln Ala Leu Gly Leu Pro Glu
 50 55 60
- Asn Val Leu Asp Ala Pro Ala Cys Ala Val Glu Phe Ile His Val Tyr 65 70 75 80
- Ser Leu Ile His Asp Asp Leu Pro Ala Met Asp Asn Asp Asp Leu Arg 85 90 95
- Arg Gly Lys Pro Thr Cys His Lys Ala Tyr Asp Glu Ala Thr Ala Ile 100 105 110
- Leu Ala Gly Asp Ala Leu Gln Ala Leu Ala Phe Glu Val Leu Ala Asn 115 120 125
- Asp Pro Gly Ile Thr Val Asp Ala Pro Ala Arg Leu Lys Met Ile Thr 130 135 140
- Ala Leu Thr Arg Ala Ser Gly Ser Gln Gly Met Val Gly Gln Ala 145 150 155 160
- Ile Asp Leu Gly Ser Val Gly Arg Lys Leu Thr Leu Pro Glu Leu Glu
 165 170 175
- Asn Met His Ile His Lys Thr Gly Ala Leu Ile Arg Ala Ser Val Asn 180 185 190
- Leu Ala Ala Leu Ser Lys Pro Asp Leu Asp Thr Cys Val Ala Lys Lys 195 200 205
- Leu Asp His Tyr Ala Lys Cys Ile Gly Leu Ser Phe Gln Val Lys Asp 210 215 220
- Asp Ile Leu Asp Ile Glu Ala Asp Thr Ala Thr Leu Gly Lys Thr Gln 225 230 235 240
- Gly Lys Asp Ile Asp Asn Asp Lys Pro Thr Tyr Pro Ala Leu Leu Gly
 245 250 255
- Met Ala Gly Ala Lys Gln Lys Ala Gln Glu Leu His Glu Gln Ala Val 260 265 270
- Glu Ser Leu Thr Gly Phe Gly Ser Glu Ala Asp Leu Leu Arg Glu Leu 275 280 285

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Ser Leu Tyr Ile Ile Glu Arg Thr His
    290
<210> 15
<211> 1533
<212> DNA
<213> Methylomonas 16a
<220>
<223> ORF8
<400> 15
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atgttgctga gccagcgcgg cttcaaggta tcgattttcg acaaacatgc agaaatcggc
                                                                   120
ggccgcaacc gcccgatcaa catgaacggc tttaccttcg ataccggtcc gacattcttg
                                                                   180
ttgatgaaag gcgtgctgga cgaaatgttc gaactgtgcg agcgccgtag cgaggattat
                                                                   240
ctggaattcc tgccgctaag cccgatgtac cgcctgctgt acgacgaccg cgacatcttc
                                                                   300
gtctattccg accgcgagaa catgcgcgcc gaattgcaac gggtattcga cgaaggcacg
                                                                   360
gacggctacg aacagttcat ggaacaggaa cgcaaacgct tcaacgcgct gtatccctgc 420
atcaccegeg attattecag cetgaaatee tttttgtege tggaettgat caaggeeetg 480
ccgtggctgg cttttccgaa aagcgtgttc aataatctcg gccagtattt caaccaggaa 540
aaaatgcgcc tggccttttg ctttcagtcc aagtatctgg gcatgtcgcc gtgggaatgc
                                                                   600
ceggeactgt ttacgatget gecetatetg gageacgaat aeggeattta teaegteaaa 660
ggcggcctga accgcatcgc ggcggcgatg gcgcaagtga tcgcggaaaa cggcggcgaa 720
attcacttga acagcgaaat cgagtcgctg atcatcgaaa acggcgctgc caagggcgtc
                                                                   780
aaattacaac atggcgcgga gctgcgcggc gacgaagtca tcatcaacgc ggattttgcc
cacgcgatga cgcatctggt caaaccgggc gtcttgaaaa aatacacccc ggaaaacctg
                                                                   900
aagcagcgcg agtattcctg ttcgaccttc atgctgtatc tqqqtttqqa caaqatttac
gatetgeege accataceat egtgtttgee aaggattaca ceaceaatat eegeaacatt 1020
ttcgacaaca aaaccctgac ggacgatttt tcgttttacg tgcaaaacgc cagcgccagc 1080
gacgacagee tagegeeage eggeaaateg gegetgtaeg tgetggtgee gatgeeeaae 1140
aacgacagcg gcctggactg gcaggcgcat tgccaaaacg tgcgcgaaca ggtgttggac 1200
acgctgggcg cgcgactggg attgagcgac atcaqagccc atatcqaatq cqaaaaaatc 1260
atcacgccgc aaacctggga aacggacgaa cacgtttaca agggcgccac tttcagtttg 1320
tegeacaagt teageeaaat getgtaetgg eggeegeaca acegtttega ggaactggee 1380
aattgctatc tggtcggcgg cggcacgcat cccggtagcg gtttgccgac catctacgaa 1440
teggegegga ttteggeeaa getgatttee cagaaacate gggtgaggtt caaggacata 1500
gcacacagcg cctggctgaa aaaagccaaa gcc
                                                                  1533
<210> 16
<211> 511
<212> PRT
<213> Methylomonas 16a
<223> Amino acid sequences encoded by ORF8
<400> 16
Met Ala Asn Thr Lys His Ile Ile Ile Val Gly Ala Gly Pro Gly Gly
Leu Cys Ala Gly Met Leu Leu Ser Gln Arg Gly Phe Lys Val Ser Ile
             20
Phe Asp Lys His Ala Glu Ile Gly Gly Arg Asn Arg Pro Ile Asn Met
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- Asn Gly Phe Thr Phe Asp Thr Gly Pro Thr Phe Leu Leu Met Lys Gly 50 55 60

 Val Leu Asp Glu Met Phe Glu Leu Cys Glu Arg Arg Ser Glu Asp Tyr
- Leu Glu Phe Leu Pro Leu Ser Pro Met Tyr Arg Leu Leu Tyr Asp Asp 85 90 95
- Arg Asp Ile Phe Val Tyr Ser Asp Arg Glu Asn Met Arg Ala Glu Leu 100 105 110
- Gln Arg Val Phe Asp Glu Gly Thr Asp Gly Tyr Glu Gln Phe Met Glu
- Gln Glu Arg Lys Arg Phe Asn Ala Leu Tyr Pro Cys Ile Thr Arg Asp 130 135 140
- Tyr Ser Ser Leu Lys Ser Phe Leu Ser Leu Asp Leu Ile Lys Ala Leu 145 150 155 160
- Pro Trp Leu Ala Phe Pro Lys Ser Val Phe Asn Asn Leu Gly Gln Tyr 165 170 175
- Phe Asn Gln Glu Lys Met Arg Leu Ala Phe Cys Phe Gln Ser Lys Tyr 180 185 190
- Leu Gly Met Ser Pro Trp Glu Cys Pro Ala Leu Phe Thr Met Leu Pro 195 200 205
- Tyr Leu Glu His Glu Tyr Gly Ile Tyr His Val Lys Gly Gly Leu Asn 210 215 220
- Arg Ile Ala Ala Ala Met Ala Gln Val Ile Ala Glu Asn Gly Glu 225 230 235 240
- Ile His Leu Asn Ser Glu Ile Glu Ser Leu Ile Glu Asn Gly Ala
- Ala Lys Gly Val Lys Leu Gln His Gly Ala Glu Leu Arg Gly Asp Glu 260 265 270
- Val Ile Ile Asn Ala Asp Phe Ala His Ala Met Thr His Leu Val Lys 275 280 285
- Pro Gly Val Leu Lys Lys Tyr Thr Pro Glu Asn Leu Lys Gln Arg Glu 290 295 300
- Tyr Ser Cys Ser Thr Phe Met Leu Tyr Leu Gly Leu Asp Lys Ile Tyr 305 310 315 320
- Asp Leu Pro His His Thr Ile Val Phe Ala Lys Asp Tyr Thr Thr Asn 325 330 335
- Ile Arg Asn Ile Phe Asp Asn Lys Thr Leu Thr Asp Asp Phe Ser Phe 340 345 350
- Tyr Val Gln Asn Ala Ser Ala Ser Asp Asp Ser Leu Ala Pro Ala Gly 355 360 365

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Lys Ser Ala Leu Tyr Val Leu Val Pro Met Pro Asn Asn Asp Ser Gly
Leu Asp Trp Gln Ala His Cys Gln Asn Val Arg Glu Gln Val Leu Asp
385
                    390
                                        395
Thr Leu Gly Ala Arg Leu Gly Leu Ser Asp Ile Arg Ala His Ile Glu
Cys Glu Lys Ile Ile Thr Pro Gln Thr Trp Glu Thr Asp Glu His Val
                                425
                                                    430
Tyr Lys Gly Ala Thr Phe Ser Leu Ser His Lys Phe Ser Gln Met Leu
Tyr Trp Arg Pro His Asn Arg Phe Glu Glu Leu Ala Asn Cys Tyr Leu
                        455
Val Gly Gly Gly Thr His Pro Gly Ser Gly Leu Pro Thr Ile Tyr Glu
                                        475
Ser Ala Arg Ile Ser Ala Lys Leu Ile Ser Gln Lys His Arg Val Arg
                                    490
Phe Lys Asp Ile Ala His Ser Ala Trp Leu Lys Lys Ala Lys Ala
                                505
<210> 17
<211> 1491
<212> DNA
<213> Methylomonas 16a
<220>
<223> ORF9
<400> 17
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gccgctattt cgctggccac ggccggcttt tccgtgcaac tcatcgaaaa aaacgacaag
                                                                   120
gteggeggea ageteaacat catgaceaaa gaeggettta cettegatet ggggeegtee
                                                                   180
attttgacga tgccgcacat ctttgaggcc ttgttcacag gggccggcaa aaacatggcc
                                                                   240
gattacgtgc aaatccagaa agtcgaaccg cactggcgca atttcttcga ggacggtagc
                                                                   300
gtgatcgact tgtgcgaaga cgccgaaacc cagcgccgcg agctggataa acttggcccc
                                                                   360
ggcacttacg cgcaattcca gcgctttctg gactattcga aaaacctctg cacggaaacc
                                                                   420
gaagccggtt acttcgccaa gggcctggac ggcttttggg atttactcaa gttttacggc
                                                                   480
ccgctccgca gcctgctgag tttcgacgtc ttccgcagca tggaccaggg cgtgcgccgc
                                                                   540
tttatttccg atcccaagtt ggtcgaaatc ctgaattact tcatcaaata cqtcqqctcc
                                                                   600
tegeettaeg atgegeege ettgatgaac etgetgeett acatteaata teattaegge
                                                                   660
ctgtggtacg tgaaaggcgg catgtatggc atggcgcagg ccatggaaaa actggccgtg
                                                                   720
gaattgggcg tcgagattcg tttagatgcc gaggtgtcgg aaatccaaaa acaggacggc
                                                                   780
agagcctgcg ccgtaaagtt ggcgaacggc gacgtgctgc cggccgacat cgtggtgtcg
                                                                   840
aacatggaag tgattccggc gatggaaaaa ctgctgcgca gcccggccag cgaactgaaa
                                                                   900
aaaatgcagc gcttcgagcc tagctgttcc ggcctggtgc tgcacttggg cgtggacagg
                                                                   960
ctgtatccgc aactggcgca ccacaatttc ttttattccg atcatccgcg cgaacatttc 1020
gatgcggtat tcaaaagcca tcgcctgtcg gacgatccga ccatttatct ggtcgcgccg 1080
tgcaagaccg accccgccca ggcgccggcc ggctgcgaga tcatcaaaat cctgcccat 1140
atcccgcacc tcgaccccga caaactgctg accgccgagg attattcagc cttgcgcgag 1200
cgggtgctgg tcaaactcga acgcatgggc ctgacggatt tacgccaaca catcgtgacc 1260
gaagaatact ggacgccgct ggatattcag gccaaatatt attcaaacca gggctcgatt 1320
tacggcgtgg tcgccgaccg cttcaaaaac ctgggtttca aggcacctca acgcagcagc 1380
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<210> 18

<211> 497

<212> PRT

<213> Methylomonas 16a

<220>

<223> Amino acid sequences encoded by ORF9

<400> 18

Met Asn Ser Asn Asp Asn Gln Arg Val Ile Val Ile Gly Ala Gly Leu

1 5 10 15

Gly Gly Leu Ser Ala Ala Ile Ser Leu Ala Thr Ala Gly Phe Ser Val 20 25 30

Gln Leu Ile Glu Lys Asn Asp Lys Val Gly Gly Lys Leu Asn Ile Met 35 40 45

Thr Lys Asp Gly Phe Thr Phe Asp Leu Gly Pro Ser Ile Leu Thr Met 50 55 60

Pro His Ile Phe Glu Ala Leu Phe Thr Gly Ala Gly Lys Asn Met Ala 65 70 75 80

Asp Tyr Val Gln Ile Gln Lys Val Glu Pro His Trp Arg Asn Phe Phe
85 90 95

Glu Asp Gly Ser Val Ile Asp Leu Cys Glu Asp Ala Glu Thr Gln Arg 100 105 110

Arg Glu Leu Asp Lys Leu Gly Pro Gly Thr Tyr Ala Gln Phe Gln Arg 115 120 125

Phe Leu Asp Tyr Ser Lys Asn Leu Cys Thr Glu Thr Glu Ala Gly Tyr 130 135 140

Phe Ala Lys Gly Leu Asp Gly Phe Trp Asp Leu Leu Lys Phe Tyr Gly
145 150 155 160

Pro Leu Arg Ser Leu Leu Ser Phe Asp Val Phe Arg Ser Met Asp Gln 165 170 175

Gly Val Arg Arg Phe Ile Ser Asp Pro Lys Leu Val Glu Ile Leu Asn 180 185 190

Tyr Phe Ile Lys Tyr Val Gly Ser Ser Pro Tyr Asp Ala Pro Ala Leu 195 200 205

Met Asn Leu Leu Pro Tyr Ile Gln Tyr His Tyr Gly Leu Trp Tyr Val 210 215 220

Lys Gly Gly Met Tyr Gly Met Ala Gln Ala Met Glu Lys Leu Ala Val 225 230 235 240

Glu Leu Gly Val Glu Ile Arg Leu Asp Ala Glu Val Ser Glu Ile Gln 245 250 255 Lys Gln Asp Gly Arg Ala Cys Ala Val Lys Leu Ala Asn Gly Asp Val 260 265 270

Leu Pro Ala Asp Ile Val Val Ser Asn Met Glu Val Ile Pro Ala Met 275 280 285

Glu Lys Leu Leu Arg Ser Pro Ala Ser Glu Leu Lys Lys Met Gln Arg 290 295 300

Phe Glu Pro Ser Cys Ser Gly Leu Val Leu His Leu Gly Val Asp Arg 305 310 315 320

Leu Tyr Pro Gln Leu Ala His His Asn Phe Phe Tyr Ser Asp His Pro 325 330 335

Arg Glu His Phe Asp Ala Val Phe Lys Ser His Arg Leu Ser Asp Asp 340 345 350

Pro Thr Ile Tyr Leu Val Ala Pro Cys Lys Thr Asp Pro Ala Gln Ala 355 360 365

Pro Ala Gly Cys Glu Ile Ile Lys Ile Leu Pro His Ile Pro His Leu 370 375 380

Asp Pro Asp Lys Leu Leu Thr Ala Glu Asp Tyr Ser Ala Leu Arg Glu 385 390 395 400

Arg Val Leu Val Lys Leu Glu Arg Met Gly Leu Thr Asp Leu Arg Gln
405 410 415

His Ile Val Thr Glu Glu Tyr Trp Thr Pro Leu Asp Ile Gln Ala Lys
420 425 430

Tyr Tyr Ser Asn Gln Gly Ser Ile Tyr Gly Val Val Ala Asp Arg Phe 435 440 445

Lys Asn Leu Gly Phe Lys Ala Pro Gln Arg Ser Ser Glu Leu Ser Asn 450 455 460

Leu Tyr Phe Val Gly Gly Ser Val Asn Pro Gly Gly Gly Met Pro Met 465 470 475 480

Val Thr Leu Ser Gly Gln Leu Val Arg Asp Lys Ile Val Ala Asp Leu 485 490 495

Gln

<210> 19

<211> 22

<212> DNA

<213> Artificial Sequence

-220-

<223> Description of Artificial Sequence:primer

<400> 19

aaggatccgc gtattcgtac tc

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<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:primer
<400> 20
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                                                                    40
<210> 21
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:primer
<400> 21
aaggatccta ctcgagctga catcagtgct
                                                                    30
<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence:primer
<400> 22
gctctagatg caaccagaat cg
                                                                    22
<210> 23
<211> 954
<212> DNA
<213> Methylomonas 16a
<400> 23
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attgtcgatc aagccatcga agcctttggt gcgccgattt atgtgcggca cgaggtggtg 120
cataaccgca ccgtggtcga tggactgaaa caaaaaggtg cggtgttcat cgaggaacta 180
agcgatgtgc cggtgggttc ctacttgatt ttcagcgcgc acggcgtatc caaggaggtg 240
caacaggaag ccgaggagcg ccagttgacg gtattcgatg cgacttgtcc gctggtgacc 300
aaagtgcaca tgcaggttgc caagcatgcc aaacagggcc gagaagtgat tttgatcggc 360
cacgccggtc atccggaagt ggaaggcacg atgggccagt atgaaaaatg caccgaaggc 420
ggcggcattt atctggtcga aactccggaa gacgtacgca atttgaaagt caacaatccc 480
aatgatctgg cctatgtgac gcagacgacc ttgtcgatga ccgacaccaa ggtcatggtg 540
gatgcgttac gcgaacaatt tccgtccatt aaggagcaaa aaaaggacga tatttgttac 600
gcgacgcaaa accgtcagga tgcggtgcat gatctggcca agatttccga cctgattctg 660
gttgtcggct ctcccaatag ttcgaattcc aaccgtttgc gtgaaatcgc cgtgcaactc 720
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gaggaaaagg tagtcttttc gattcccaag gagttgaaaa aacatatgca aqcg
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- <210> 24
- <211> 318
- <212> PRT
- <213> Methylomonas 16a
- <400> 24
- Met Gln Ile Val Leu Ala Asn Pro Arg Gly Phe Cys Ala Gly Val Asp 1 5 10 15
- Arg Ala Ile Glu Ile Val Asp Gln Ala Ile Glu Ala Phe Gly Ala Pro 20 25 30
- Ile Tyr Val Arg His Glu Val Val His Asn Arg Thr Val Val Asp Gly 35 40 45
- Leu Lys Gln Lys Gly Ala Val Phe Ile Glu Glu Leu Ser Asp Val Pro
 50 55 60
- Val Gly Ser Tyr Leu Ile Phe Ser Ala His Gly Val Ser Lys Glu Val 65 70 75 80
- Gln Gln Glu Ala Glu Glu Arg Gln Leu Thr Val Phe Asp Ala Thr Cys
 85 90 95
- Pro Leu Val Thr Lys Val His Met Gln Val Ala Lys His Ala Lys Gln
 100 105 110
- Gly Arg Glu Val Ile Leu Ile Gly His Ala Gly His Pro Glu Val Glu
 115 120 125
- Gly Thr Met Gly Gln Tyr Glu Lys Cys Thr Glu Gly Gly Gly Ile Tyr 130 135 140
- Leu Val Glu Thr Pro Glu Asp Val Arg Asn Leu Lys Val Asn Asn Pro 145 150 155 160
- Asn Asp Leu Ala Tyr Val Thr Gln Thr Thr Leu Ser Met Thr Asp Thr 165 170 175
- Lys Val Met Val Asp Ala Leu Arg Glu Gln Phe Pro Ser Ile Lys Glu 180 185 190
- Gln Lys Lys Asp Asp Ile Cys Tyr Ala Thr Gln Asn Arg Gln Asp Ala 195 200 205
- Val His Asp Leu Ala Lys Ile Ser Asp Leu Ile Leu Val Val Gly Ser 210 215 220
- Pro Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu Ile Ala Val Gln Leu 225 230 235 240
- Gly Lys Pro Ala Tyr Leu Ile Asp Thr Tyr Gln Asp Leu Lys Gln Asp 245 250 255
- Trp Leu Glu Gly Ile Glu Val Val Gly Val Thr Ala Gly Ala Ser Ala 260 265 270

Pro Glu Val Leu Val Gln Glu Val Ile Asp Gln Leu Lys Ala Trp Gly 275 280 285

Gly Glu Thr Thr Ser Val Arg Glu Asn Ser Gly Ile Glu Glu Lys Val 290 295 300

Val Phe Ser Ile Pro Lys Glu Leu Lys Lys His Met Gln Ala 305 310 315